FIG.1

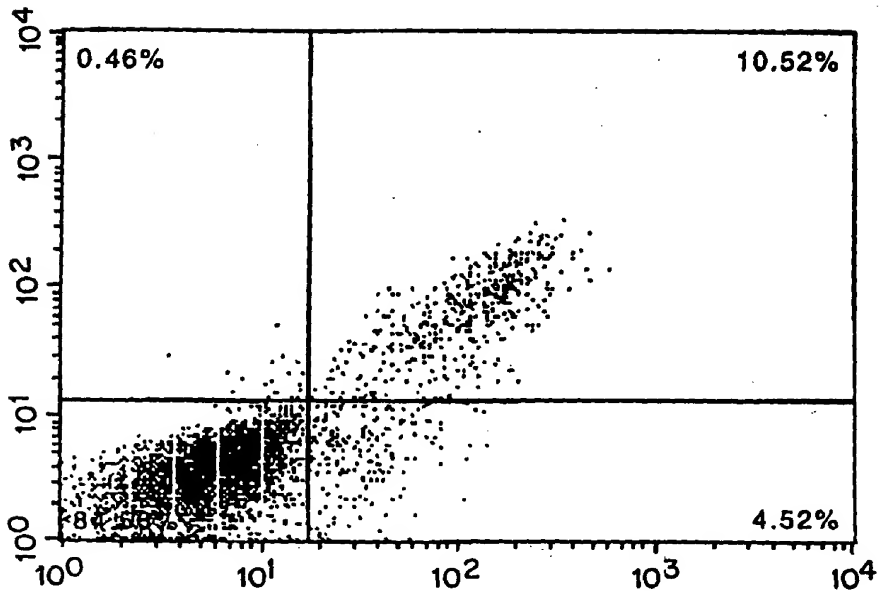


FIG. 2

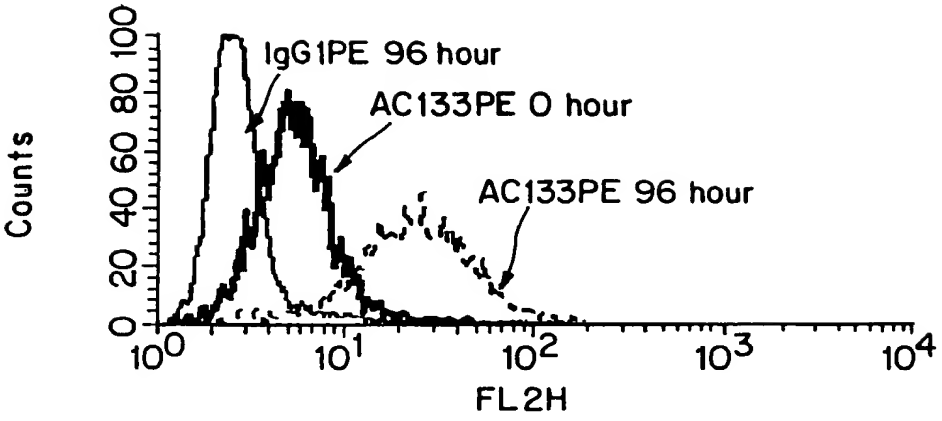

IgG1PE 96 hour
AC133PE 0 hour
AC133PE 96 hour
Counts
0 20 40 60 80 100
10^0 10^1 10^2 10^3 10^4
FL2H

FIG. 3

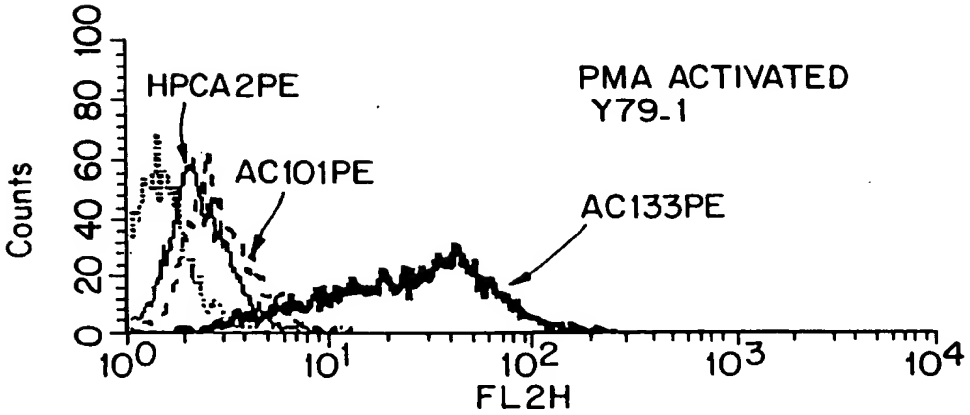

HPCA2PE
AC101PE
PMA ACTIVATED
Y79-1
AC133PE
Counts
0 20 40 60 80 100
10^0 10^1 10^2 10^3 10^4
FL2H

FIG.4A

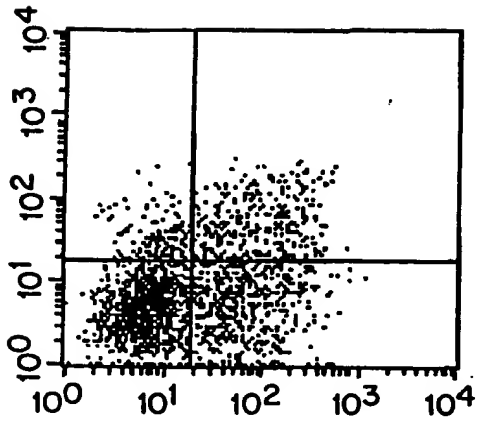


FIG.4B

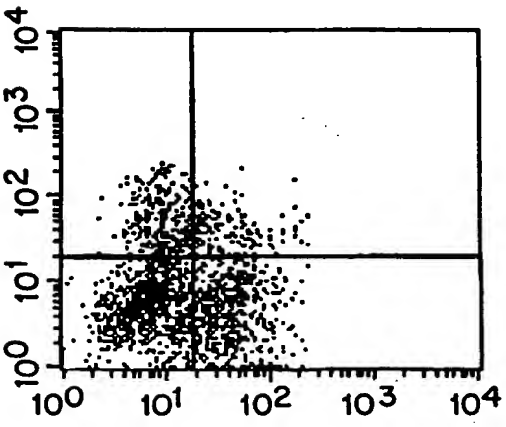


FIG.5A

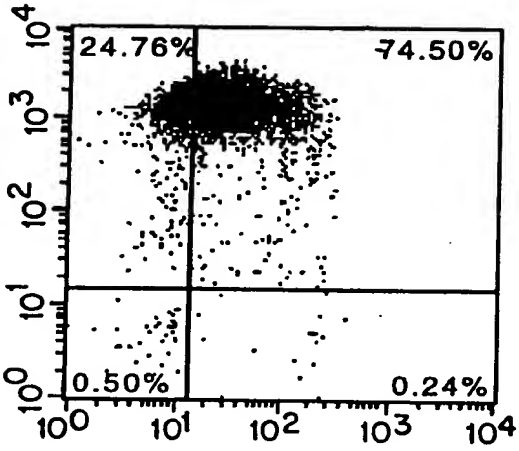


FIG.5B

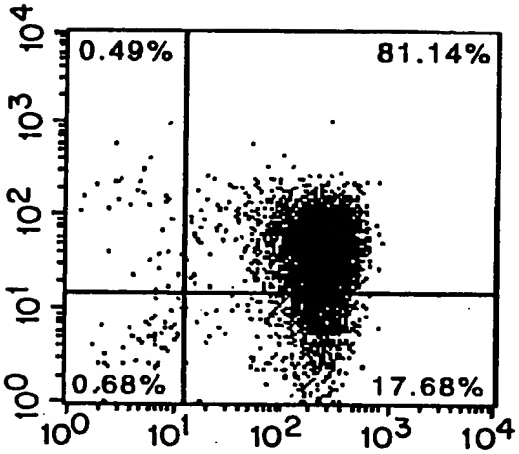


FIG.5C

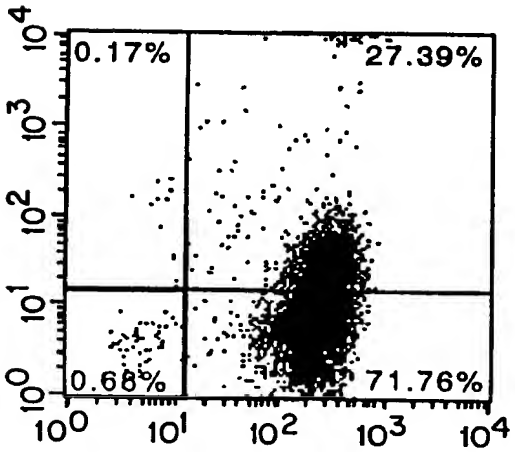


FIG.5D

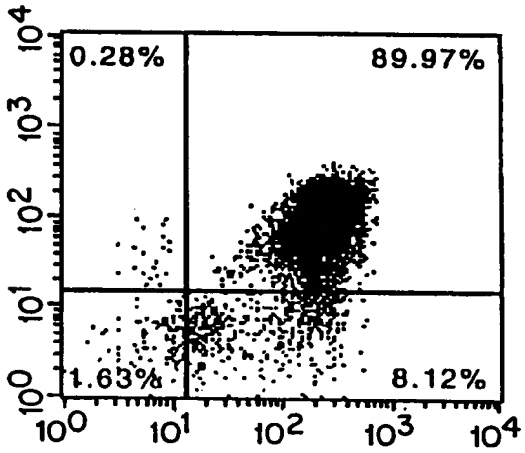


FIG.6

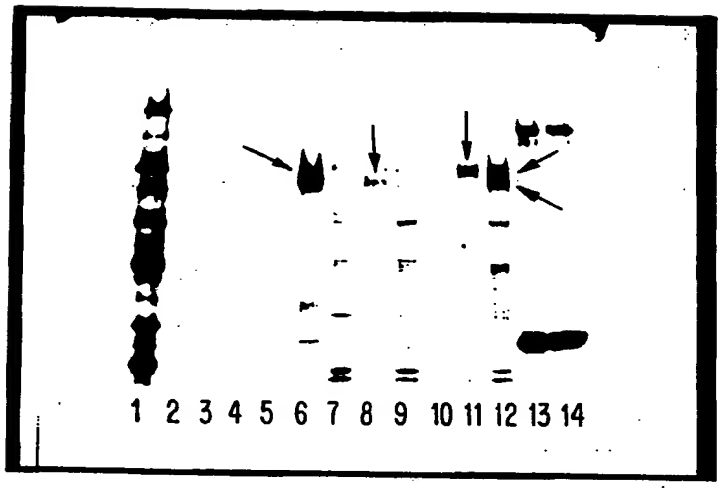


FIG. 7A

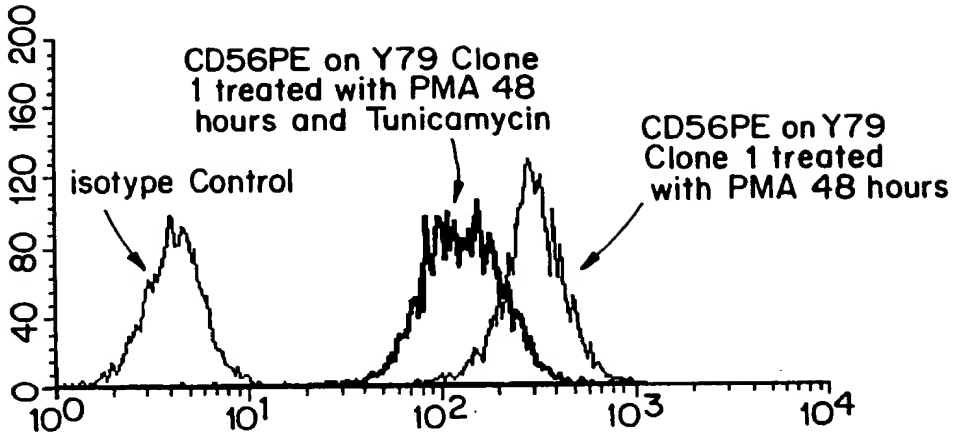

CD56PE on Y79 Clone 1 treated with PMA 48 hours and Tunicamycin
CD56PE on Y79 Clone 1 treated with PMA 48 hours
isotype Control
0
40
80
120
160
200
10^0
10^1
10^2
10^3
10^4

FIG. 7B

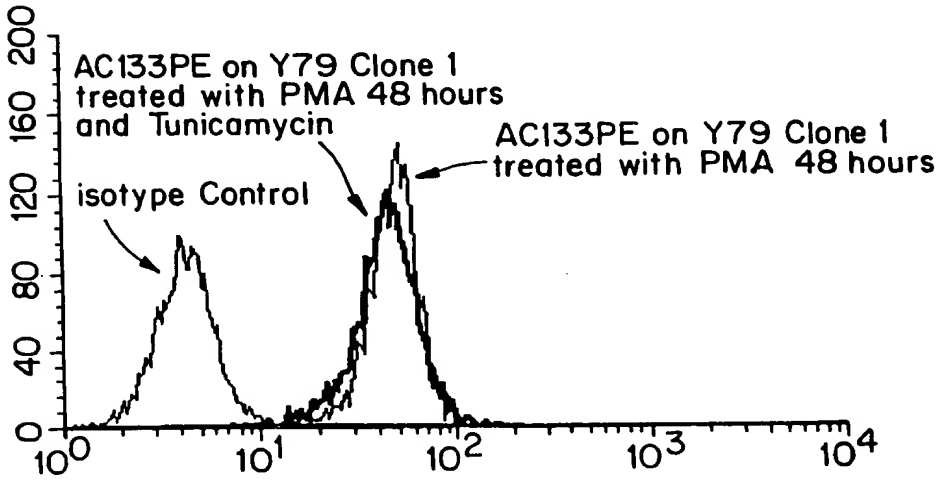

AC133PE on Y79 Clone 1 treated with PMA 48 hours and Tunicamycin
AC133PE on Y79 Clone 1 treated with PMA 48 hours
isotype Control
0
40
80
120
160
200
10^0
10^1
10^2
10^3
10^4

FIG.8

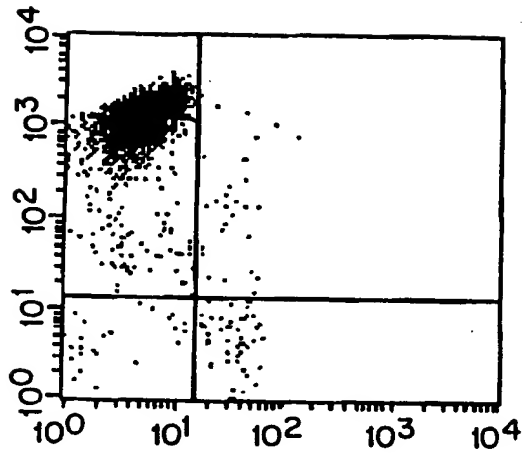


FIG.9A

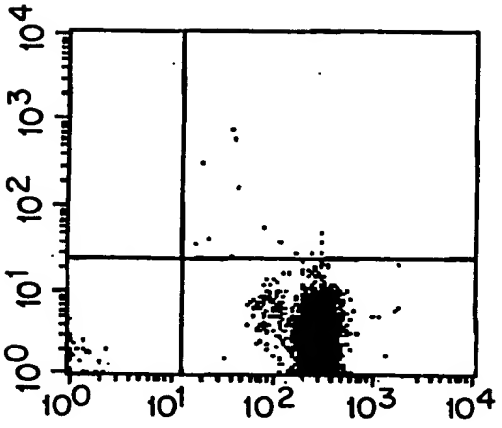

10^4
10^3
10^2
10^1
10^0
10^0
10^1
10^2
10^3
10^4

FIG.9B

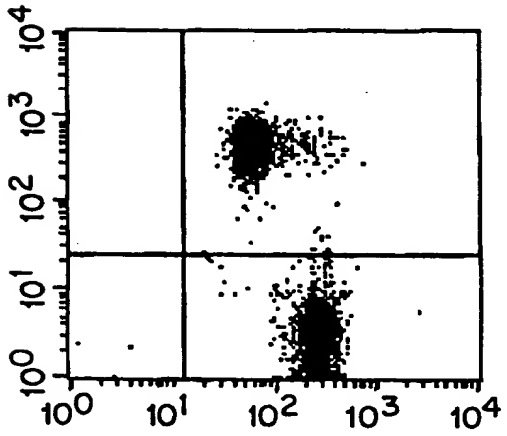

10^4
10^3
10^2
10^1
10^0
10^0
10^1
10^2
10^3
10^4

FIG.10

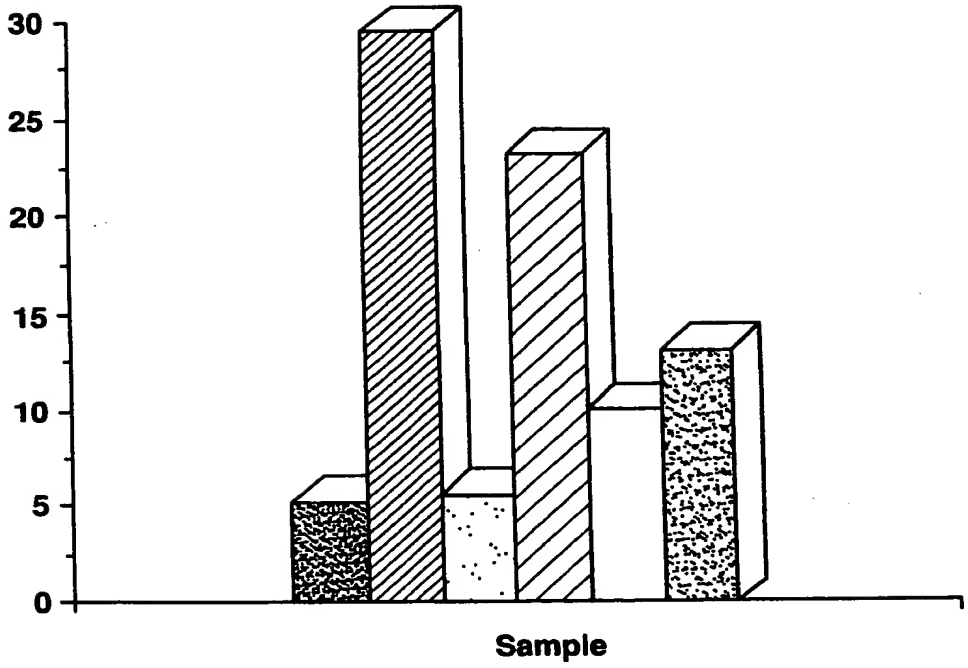

30
25
20
15
10
5
0
Sample
LP Control/CFU-GM
LP Control/BFU-E
C4-AC101/CFU-GM
C4-AC101/BFU-E
C4-AC133/CFU-GM
C4-AC133/BFU-E

FIG.11

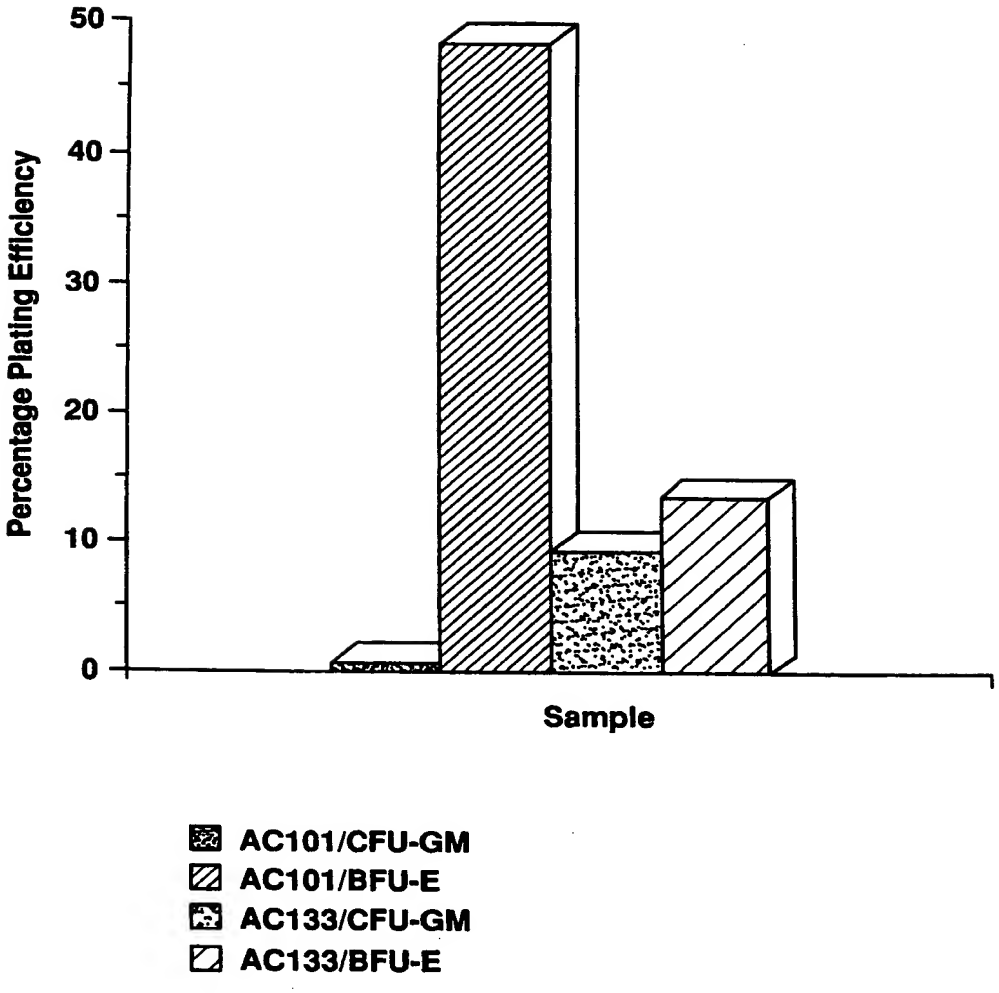

50
40
30
20
10
0
Percentage Plating Efficiency
Sample
AC101/CFU-GM
AC101/BFU-E
AC133/CFU-GM
AC133/BFU-E

FIG.12-1

```
CCAAGTTCTA CCTCATGTTT GGAGGATCTT GCTAGCT ATG GCC CTC GTA CTC GGC        55
                                          Met Ala Leu Val Leu Gly
                                            1               5

TCC CTG TTG CTG CTG GGG CTG TGC GGG AAC TCC TTT TCA GGA GGG CAG        103
Ser Leu Leu Leu Leu Gly Leu Cys Gly Asn Ser Phe Ser Gly Gly Gln
            10                  15                  20

CCT TCA TCC ACA GAT GCT CCT AAG GCT TGG AAT TAT GAA TTG CCT GCA        151
Pro Ser Ser Thr Asp Ala Pro Lys Ala Trp Asn Tyr Glu Leu Pro Ala
        25                  30                  35

ACA AAT TAT GAG ACC CAA GAC TCC CAT AAA GCT GGA CCC ATT GGC ATT        199
Thr Asn Tyr Glu Thr Gln Asp Ser His Lys Ala Gly Pro Ile Gly Ile
    40                  45                  50

CTC TTT GAA CTA GTG CAT ATC TTT CTC TAT GTG GTA CAG CCG CGT GAT        247
Leu Phe Glu Leu Val His Ile Phe Leu Tyr Val Val Gln Pro Arg Asp
55                  60                  65                  70

TTC CCA GAA GAT ACT TTG AGA AAA TTC TTA CAG AAG GCA TAT GAA TCC        295
Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu Gln Lys Ala Tyr Glu Ser
                75                  80                  85

AAA ATT GAT TAT GAC AAG CCA GAA ACT GTA ATC TTA GGT CTA AAG ATT        343
Lys Ile Asp Tyr Asp Lys Pro Glu Thr Val Ile Leu Gly Leu Lys Ile
            90                  95                  100

GTC TAC TAT GAA GCA GGG ATT ATT CTA TGC TGT GTC CTG GGG CTG CTG        391
Val Tyr Tyr Glu Ala Gly Ile Ile Leu Cys Cys Val Leu Gly Leu Leu
        105                 110                 115

TTT ATT ATT CTG ATG CCT CTG GTG GGG TAT TTC TTT TGT ATG TGT CGT        439
Phe Ile Ile Leu Met Pro Leu Val Gly Tyr Phe Phe Cys Met Cys Arg
    120                 125                 130

TGC TGT AAC AAA TGT GGT GGA GAA ATG CAC CAG CGA CAG AAG GAA AAT        487
Cys Cys Asn Lys Cys Gly Gly Glu Met His Gln Arg Gln Lys Glu Asn
135                 140                 145                 150

GGG CCC TTC CTG AGG AAA TGC TTT GCA ATC TCC CTG TTG GTG ATT TGT        535
Gly Pro Phe Leu Arg Lys Cys Phe Ala Ile Ser Leu Leu Val Ile Cys
                155                 160                 165

ATA ATA ATA AGC ATT GGC ATC TTC TAT GGT TTT GTG GCA AAT CAC CAG        583
Ile Ile Ile Ser Ile Gly Ile Phe Tyr Gly Phe Val Ala Asn His Gln
            170                 175                 180

GTA AGA ACC CGG ATC AAA AGG AGT CGG AAA CTG GCA GAT AGC AAT TTC        631
Val Arg Thr Arg Ile Lys Arg Ser Arg Lys Leu Ala Asp Ser Asn Phe
        185                 190                 195

AAG GAC TTG CGA ACT CTC TTG AAT GAA ACT CCA GAG CAA ATC AAA TAT        679
Lys Asp Leu Arg Thr Leu Leu Asn Glu Thr Pro Glu Gln Ile Lys Tyr
    200                 205                 210

ATA TTG GCC CAG TAC AAC ACT ACC AAG GAC AAG GCG TTC ACA GAT CTG        727
Ile Leu Ala Gln Tyr Asn Thr Thr Lys Asp Lys Ala Phe Thr Asp Leu
215                 220                 225                 230
```

FIG.12-2

```
AAC AGT ATC AAT TCA GTG CTA GGA GGC GGA ATT CTT GAC CGA CTG AGA    775
Asn Ser Ile Asn Ser Val Leu Gly Gly Gly Ile Leu Asp Arg Leu Arg
                235                 240                 245

CCC AAC ATC ATC CCT GTT CTT GAT GAG ATT AAG TCC ATG GCA ACA GCG    823
Pro Asn Ile Ile Pro Val Leu Asp Glu Ile Lys Ser Met Ala Thr Ala
            250                 255                 260

ATC AAG GAG ACC AAA GAG GCG TTG GAG AAC ATG AAC AGC ACC TTG AAG    871
Ile Lys Glu Thr Lys Glu Ala Leu Glu Asn Met Asn Ser Thr Leu Lys
        265                 270                 275

AGC TTG CAC CAA CAA AGT ACA CAG CTT AGC AGC AGT CTG ACC AGC GTG    919
Ser Leu His Gln Gln Ser Thr Gln Leu Ser Ser Ser Leu Thr Ser Val
    280                 285                 290

AAA ACT AGC CTG CGG TCA TCT CTC AAT GAC CCT CTG TGC TTG GTG CAT    967
Lys Thr Ser Leu Arg Ser Ser Leu Asn Asp Pro Leu Cys Leu Val His
295                 300                 305                 310

CCA TCA AGT GAA ACC TGC AAC AGC ATC AGA TTG TCT CTA AGC CAG CTG   1015
Pro Ser Ser Glu Thr Cys Asn Ser Ile Arg Leu Ser Leu Ser Gln Leu
                315                 320                 325

AAT AGC AAC CCT GAA CTG AGG CAG CTT CCA CCC GTG GAT GCA GAA CTT   1063
Asn Ser Asn Pro Glu Leu Arg Gln Leu Pro Pro Val Asp Ala Glu Leu
            330                 335                 340

GAC AAC GTT AAT AAC GTT CTT AGG ACA GAT TTG GAT GGC CTG GTC CAA   1111
Asp Asn Val Asn Asn Val Leu Arg Thr Asp Leu Asp Gly Leu Val Gln
        345                 350                 355

CAG GGC TAT CAA TCC CTT AAT GAT ATA CCT GAC AGA GTA CAA CGC CAA   1159
Gln Gly Tyr Gln Ser Leu Asn Asp Ile Pro Asp Arg Val Gln Arg Gln
    360                 365                 370

ACC ACG ACT GTC GTA GCA GGT ATC AAA AGG GTC TTG AAT TCC ATT GGT   1207
Thr Thr Thr Val Val Ala Gly Ile Lys Arg Val Leu Asn Ser Ile Gly
375                 380                 385                 390

TCA GAT ATC GAC AAT GTA ACT CAG CGT CTT CCT ATT CAG GAT ATA CTC   1255
Ser Asp Ile Asp Asn Val Thr Gln Arg Leu Pro Ile Gln Asp Ile Leu
                395                 400                 405

TCA GCA TTC TCT GTT TAT GTT AAT AAC ACT GAA AGT TAC ATC CAC AGA   1303
Ser Ala Phe Ser Val Tyr Val Asn Asn Thr Glu Ser Tyr Ile His Arg
            410                 415                 420

AAT TTA CCT ACA TTG GAA GAG TAT GAT TCA TAC TGG TGG CTG GGT GGC   1351
Asn Leu Pro Thr Leu Glu Glu Tyr Asp Ser Tyr Trp Trp Leu Gly Gly
        425                 430                 435

CTG GTC ATC TGC TCT CTG CTG ACC CTC ATC GTG ATT TTT TAC TAC CTG   1399
Leu Val Ile Cys Ser Leu Leu Thr Leu Ile Val Ile Phe Tyr Tyr Leu
    440                 445                 450

GGC TTA CTG TGT GGC GTG TGC GGC TAT GAC AGG CAT GCC ACC CCG ACC   1447
Gly Leu Leu Cys Gly Val Cys Gly Tyr Asp Arg His Ala Thr Pro Thr
455                 460                 465                 470
```

FIG. 12-3

```
ACC CGA GGC TGT GTC TCC AAC ACC GGA GGC GTC TTC CTC ATG GTT GGA      1495
Thr Arg Gly Cys Val Ser Asn Thr Gly Gly Val Phe Leu Met Val Gly
                475                 480                 485

GTT GGA TTA AGT TTC CTC TTT TGC TGG ATA TTG ATG ATC ATT GTG GTT      1543
Val Gly Leu Ser Phe Leu Phe Cys Trp Ile Leu Met Ile Ile Val Val
            490                 495                 500

CTT ACC TTT GTC TTT GGT GCA AAT GTG GAA AAA CTG ATC TGT GAA CCT      1591
Leu Thr Phe Val Phe Gly Ala Asn Val Glu Lys Leu Ile Cys Glu Pro
        505                 510                 515

TAC ACG AGC AAG GAA TTA TTC CGG GTT TTG GAT ACA CCC TAC TTA CTA      1639
Tyr Thr Ser Lys Glu Leu Phe Arg Val Leu Asp Thr Pro Tyr Leu Leu
    520                 525                 530

AAT GAA GAC TGG GAA TAC TAT CTC TCT GGG AAG CTA TTT AAT AAA TCA      1687
Asn Glu Asp Trp Glu Tyr Tyr Leu Ser Gly Lys Leu Phe Asn Lys Ser
535                 540                 545                 550

AAA ATG AAG CTC ACT TTT GAA CAA GTT TAC AGT GAC TGC AAA AAA AAT      1735
Lys Met Lys Leu Thr Phe Glu Gln Val Tyr Ser Asp Cys Lys Lys Asn
                555                 560                 565

AGA GGC ACT TAC GGC ACT CTT CAC CTG CAG AAC AGC TTC AAT ATC AGT      1783
Arg Gly Thr Tyr Gly Thr Leu His Leu Gln Asn Ser Phe Asn Ile Ser
            570                 575                 580

GAA CAT CTC AAC ATT AAT GAG CAT ACT GGA AGC ATA AGC AGT GAA TTG      1831
Glu His Leu Asn Ile Asn Glu His Thr Gly Ser Ile Ser Ser Glu Leu
        585                 590                 595

GAA AGT CTG AAG GTA AAT CTT AAT ATC TTT CTG TTG GGT GCA GCA GGA      1879
Glu Ser Leu Lys Val Asn Leu Asn Ile Phe Leu Leu Gly Ala Ala Gly
    600                 605                 610

AGA AAA AAC CTT CAG GAT TTT GCT GCT TGT GGA ATA GAC AGA ATG AAT      1927
Arg Lys Asn Leu Gln Asp Phe Ala Ala Cys Gly Ile Asp Arg Met Asn
615                 620                 625                 630

TAT GAC AGC TAC TTG GCT CAG ACT GGT AAA TCC CCC GCA GGA GTG AAT      1975
Tyr Asp Ser Tyr Leu Ala Gln Thr Gly Lys Ser Pro Ala Gly Val Asn
                635                 640                 645

CTT TTA TCA TTT GCA TAT GAT CTA GAA GCA AAA GCA AAC AGT TTG CCC      2023
Leu Leu Ser Phe Ala Tyr Asp Leu Glu Ala Lys Ala Asn Ser Leu Pro
            650                 655                 660

CCA GGA AAT TTG AGG AAC TCC CTG AAA AGA GAT GCA CAA ACT ATT AAA      2071
Pro Gly Asn Leu Arg Asn Ser Leu Lys Arg Asp Ala Gln Thr Ile Lys
        665                 670                 675

ACA ATT CAC CAG CAA CGA GTC CTT CCT ATA GAA CAA TCA CTG AGC ACT      2119
Thr Ile His Gln Gln Arg Val Leu Pro Ile Glu Gln Ser Leu Ser Thr
    680                 685                 690

CTA TAC CAA AGC GTC AAG ATA CTT CAA CGC ACA GGG AAT GGA TTG TTG      2167
Leu Tyr Gln Ser Val Lys Ile Leu Gln Arg Thr Gly Asn Gly Leu Leu
695                 700                 705                 710

GAG AGA GTA ACT AGG ATT CTA GCT TCT CTG GAT TTT GCT CAG AAC TTC      2215
Glu Arg Val Thr Arg Ile Leu Ala Ser Leu Asp Phe Ala Gln Asn Phe
                715                 720                 725
```

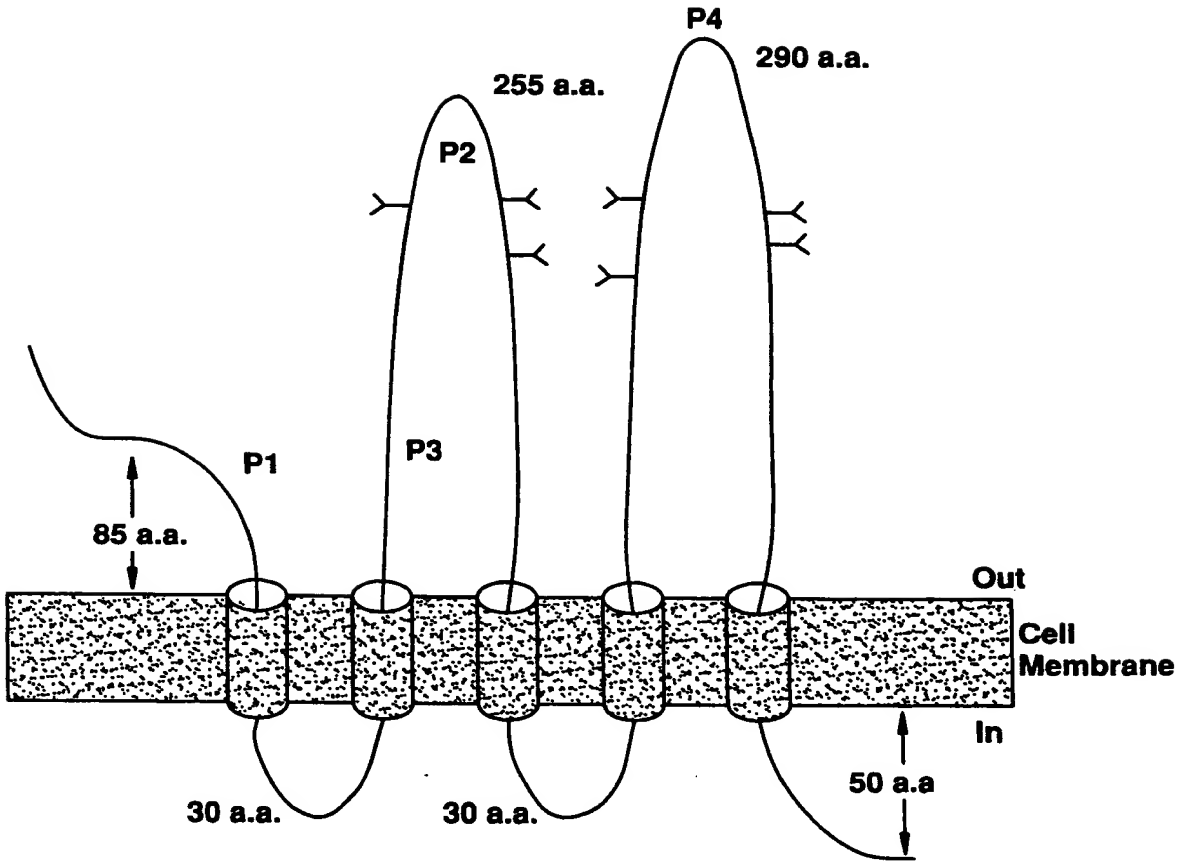
FIG. 12-4

```
ATC ACA AAC AAT ACT TCC TCT GTT ATT ATT GAG GAA ACT AAG AAG TAT      2263
Ile Thr [Asn;Asn Thr;Ser] Ser Val Ile Ile Glu Glu Thr Lys Lys Tyr
        730                       735                   740

GGG AGA ACA ATA ATA GGA TAT TTT GAA CAT TAT CTG CAG TGG ATC GAG      2311
Gly Arg Thr Ile Ile Gly Tyr Phe Glu His Tyr Leu Gln Trp Ile Glu
    745                   750                   755

TTC TCT ATC AGT GAG AAA GTG GCA TCG TGC AAA CCT GTG GCC ACC GCT      2359
Phe Ser Ile Ser Glu Lys Val Ala Ser Cys Lys Pro Val Ala Thr Ala
760                   765                   770

CTA GAT ACT GCT GTT GAT GTC TTT CTG TGT AGC TAC ATT ATC GAC CCC      2407
Leu Asp Thr Ala Val Asp Val Phe Leu Cys Ser Tyr Ile Ile Asp Pro
775                   780                   785                   790

TTG AAT TTG TTT TGG TTT GGC ATA GGA AAA GCT ACT GTA TTT TTA CTT      2455
Leu Asn Leu Phe Trp Phe Gly Ile Gly Lys Ala Thr Val Phe Leu Leu
            795                   800                   805

CCG GCT CTA ATT TTT GCG GTA AAA CTG GCT AAG TAC TAT CGT CGA ATG      2503
Pro Ala Leu Ile Phe Ala Val Lys Leu Ala Lys Tyr Tyr Arg Arg Met
        810                   815                   820

GAT TCG GAG GAC GTG TAC GAT GAT GTT GAA ACT ATA CCC ATG AAA AAT      2551
Asp Ser Glu Asp Val Tyr Asp Asp Val Glu Thr Ile Pro Met Lys Asn
    825                   830                   835

ATG GAA AAT GGT AAT AAT GGT TAT CAT AAA GAT CAT GTA TAT GGT ATT      2599
Met Glu Asn Gly Asn Asn Gly Tyr His Lys Asp His Val Tyr Gly Ile
840                   845                   850

CAC AAT CCT GTT ATG ACA AGC CCA TCA CAA CAT T GATAGCTGAT            2643
His Asn Pro Val Met Thr Ser Pro Ser Gln His
855                   860                   865

GTTGAAACTG CTTGAGCATC AGGATACTCA AAGTGGAAAG GATCACAGAT TTTTGGTAGT   2703

TTCTGGGTCT ACAAGGACTT TCCAAATCCA GGAGCAACGC CAGTGGCAAC GTAGTGACTC   2763

AGGCGGGCAC CAAGGCAACG GCACCATTGG TCTCTGGGTA GTGCTTTAAG AATGAACACA   2823

ATCACGTTAT AGTCCATGGT CCATCACTAT TCAAGGATGA CTCCCTCCCT TCCTGTCTAT   2883

TTTTGTTTTT TACTTTTTTA CACTGAGTTT CTATTTAGAC ACTACAACAT ATGGGGTGTT   2943

TGTTCCCATT GGATGCATTT CTATCAAAAC TCTATCAAAT GTGATGGCTA GATTCTAACA   3003

TATTGCCATG TGTGGAGTGT GCTGAACACA CACCAGTTTA CAGGAAAGAT GCATTTTGTG   3063

TACAGTAAAC GGTGTATATA CCTTTTGTTA CCACAGAGTT TTTTAAACAA ATGAGTATTA   3123

TAGGACTTTC TTCTAAATGA GCTAAATAAG TCACCATTGA CTTCTTGGTG CTGTTGAAAA   3183

TAATCCATTT TCACTAAAAG TGTGTGAAAC CTACAGCATA TTCTTCACGC AGAGATTTTC   3243

ATCTATTATA CTTTATCAAA GATTGGCCAT GTTCCACTTG GAAATGGCAT GCAAAAGCCA   3303

TCATAGAGAA ACCTGCGTAA CTCCATCTGA CAAATTCAAA AGAGAGAGAG AGATCTTGAG   3363

AGAGAAATGC TGTTCGTTCA AAAGTGGAGT TGTTTTAACA GATGCCAATT ACGGTGTACA   3423
```

FIG. 12-5

```
GTTTAACAGA GTTTTCTGTT GCATTAGGAT AAACATTAAT TGGAGTGCAG CTAACATGAG    3483
TATCATCAGA CTAGTATCAA GTGTTCTAAA ATGAAATATG AGAAGATCCT GTCACAATTC    3543
TTAGATCTGG TGTCCAGCAT GGATGAAACC TTTGAGTTTG GTCCCTAAAT TTGCATGAAA    3603
GCACAAGGTA AATATTCATT TGCTTCAGGA GTTTCATGTT GGATCTGTCA TTATCAAAAG    3663
TGATCAGCAA TGAAGAACTG GTCGGACAAA ATTTAACGTT GATGTAATGG AATTCCAGAT    3723
GTAGGCATTC CCCCCAGGTC TTTTCATGTG CAGATTGCAG TTCTGATTCA TTTGAATAAA    3783
AAGGAACTTG GAAAAAAAAA A                                              3804
```

FIG.13


P4
290 a.a.
255 a.a.
P2
P1
P3
85 a.a.
Out
Cell
Membrane
In
50 a.a
30 a.a.
30 a.a.